

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of:)
)
Thomas WEIMER) Group Art Unit: Unassigned
)
Serial No.: Unassigned) Examiner: Unassigned
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Filed: April 13, 2001)
)
For: PROCESS FOR FINDING)
OLIGONUCLEOTIDE)
SEQUENCES FOR NUCLEIC)
ACID AMPLIFICATION)
METHODS)

Assistant Commissioner for Patents
Washington, DC 20231

Sir:

PRELIMINARY AMENDMENT

Prior to examination of the above application, please amend this application as follows:

IN THE CLAIMS:

Please cancel claims 1-9, without prejudice or disclaimer, and replace them with new claims 10-34 as follows:

--10. (New) A process for identifying one or more heterologous oligonucleotide sequences for use in amplifying a target nucleic acid sequence comprising:

- a) selecting a target nucleic acid sequence to be amplified,
- b) fragmenting one or more conserved regions of the target nucleic acid

sequence to generate mutually overlapping oligonucleotide sequence fragments, and

c) identifying one or more heterologous oligonucleotide sequences that are similar to one or more of the mutually overlapping oligonucleotide sequence fragments, wherein the one or more heterologous oligonucleotide sequences thus identified are from a different species than the target nucleic acid sequence.

11. (New) The process of claim 10, wherein said identifying of one or more heterologous oligonucleotide sequences further comprises isolating one or more of the heterologous oligonucleotide sequences thus identified.

12. (New) The process of claim 10, wherein the one or more heterologous oligonucleotide sequences are selected from SEQ ID NOS. 1, 2, 3, 4, 5, 6, 7, 8 and 9.

13. (New) The process of claim 10, wherein the mutually overlapping oligonucleotide sequence fragments each comprise from about 1 to about 100 bases.

14. (New) The process of claim 13, wherein the mutually overlapping oligonucleotide sequence fragments each comprise from about 25 to about 75 bases.

15. (New) The process of claim 14, wherein the mutually overlapping oligonucleotide sequence fragments each comprise from about 30 to about 50 bases.

16. (New) The process of claim 15, wherein the mutually overlapping oligonucleotide sequence fragments are generated by fragmenting a conserved region of a virus genome.

17. (New) The process of claim 16, wherein the virus genome is from a Hepatitis C Virus (HCV).

18. (New) The process of claim 10, wherein the one or more heterologous oligonucleotide sequences are identified from a gene library.

19. (New) The process of claim 10, wherein the one or more heterologous oligonucleotide sequences are identified in a DNA sequence database.

20. (New) The process of claim 10, wherein said identifying of one or more heterologous oligonucleotide sequences further comprises: (i) identifying basepair mismatches between one or more of the heterologous oligonucleotide sequences and one or more of the mutually overlapping oligonucleotide sequence fragments, and (ii) replacing any mismatched base pairs thus identified in the one or more heterologous oligonucleotide sequences with a universal base.

21. (New) The process of claim 20, wherein the universal base is inosine.

22. (New) The process of claim 20, wherein one or more of the heterologous oligonucleotide sequences completely hybridize with the target nucleic acid sequence.

23. (New) The process of claim 10, further comprising using one or more of the identified heterologous oligonucleotide sequences as a primer or probe to amplify the target nucleic acid sequence.

24. (New) The process of claim 22, wherein the target nucleic acid sequence is amplified by polymerase chain reaction (PCR), nucleic acid sequence-based amplification (NASBA), transcription-mediated amplification (TMA) or ligase chain reaction (LCR).

25. (New) The process of claim 23, further comprising isolating the amplified target nucleic acid sequence.

26. (New) A reagent set for use in amplifying a nucleic acid sequence by polymerase chain reaction comprising one or more oligonucleotide primers containing one or more heterologous oligonucleotide sequences obtained according to the process of claim 10.

27. (New) The reagent set of claim 26, wherein at least one of the oligonucleotide primers is selected from SEQ ID NOS. 1, 2, 3, 4, 5, 6, 7, 8, and 9.

28. (New) The reagent set of claim 26, wherein one of the primers is labeled with a fluorescent reporter dye and a fluorescent quencher dye.

29. (New) The reagent set of claim 28, wherein the labeled primer does not hybridize completely with the target nucleic acid sequence at the 3' end.

30. (New) A reagent set for use in identifying a target nucleic acid sequence comprising an oligonucleotide probe containing one or more heterologous oligonucleotide sequences obtained according to the process of claim 10.

31. (New) The reagent set of claim 30, wherein the oligonucleotide probe is selected from SEQ ID NOS. 1, 2, 3, 4, 5, 6, 7, 8, and 9.

32. (New) The reagent set of claim 30, wherein the oligonucleotide probe carries at least two fluorescent dyes.

33. (New) The reagent set of claim 32, wherein the fluorescent dyes comprise a fluorescent reporter dye and a fluorescent quencher dye.

34. (New) The reagent set of claim 32, wherein the fluorescent dyes are located at the 5' and 3' ends of the oligonucleotide probe.--

REMARKS

With this amendment, claims 1-9 have been cancelled without prejudice or disclaimer, and new claims 10-34 have been added. If there is any fee due in connection with the filing of this Preliminary Amendment, please charge the fee to our Deposit Account No. 06-0916.

Respectfully submitted,

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Dated: April 13, 2001

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